

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 15:30:32 Search time 48 Seconds
(without alignments)
4296.941 Million cell updates/sec

Title: US-10-046-433-40

Perfect score: 1001
Sequence: 1 MAEPGSHSLARVRGRTT.....LGRSNHLPRGLMDLTQCR 1001

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database:

SPTREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriopl.*
17: sp_archaeop.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	55.3	580	4 Q9P2M2	Q9P2M2 homo sapien
2	91	9.1	300	11 Q8R215	Q8R215 mus musculu
3	15	1.5	493	4 Q96DP2	Q96DP2 homo sapien
4	8	0.8	97	10 Q42206	Q42206 arabidopsis
5	8	0.8	133	12 Q9PXT8	Q9PXT8 hepatitis c
6	8	0.8	248	10 Q9C5R4	Q9C5R4 arabidopsis
7	8	0.8	302	12 Q8V7G7	Q8V7G7 tt virus. o
8	8	0.8	353	10 Q42584	Q42584 arabidopsis
9	8	0.8	353	10 Q9SMU8	Q9SMU8 arabidopsis
10	8	0.8	430	16 Q9A0D7	Q9A0D7 streptococc
11	8	0.8	444	16 Q921L4	Q921L4 rickettsia
12	8	0.8	695	16 Q92891	Q92891 chlamydia p
13	8	0.8	695	16 Q93S58	Q93S58 chlamydia p
14	8	0.8	744	3 Q42958	Q42958 schizosach
15	7	0.7	77	5 Q95XN6	Q95XN6 caenorhabdi
16	7	0.7	79	5 Q9W2P5	Q9W2P5 drosophila

17	7	0.7	91	10 Q22823	Q22823 arabidopsis
18	7	0.7	91	10 Q9M1Z3	Q9M1Z3 arabidopsis
19	7	0.7	93	2 Q9F1P2	Q9F1P2 enterococcu
20	7	0.7	100	10 Q9XJPI	Q9XJPI aureococcus
21	7	0.7	106	16 Q97RY2	Q97RY2 streptococ
22	7	0.7	115	5 Q9N7S4	Q9N7S4 leishmania
23	7	0.7	116	10 Q9M280	Q9M280 arabidopsis
24	7	0.7	122	2 Q9RAN1	Q9RAN1 methylobact
25	7	0.7	124	5 Q94045	Q94045 caenorhabdi
26	7	0.7	132	5 Q96404	Q96404 plasmodium
27	7	0.7	134	17 Q97UE3	Q97UE3 sulfolobus
28	7	0.7	138	2 Q9EUI6	Q9EUI6 salmonella
29	7	0.7	141	2 Q05567	Q05567 mycobacteri
30	7	0.7	159	17 Q9HRJ4	Q9HRJ4 halobacteri
31	7	0.7	163	5 Q9U732	Q9U732 cryptospori
32	7	0.7	163	5 Q9G0D9	Q9G0D9 cryptospori
33	7	0.7	165	10 Q8S4A8	Q8S4A8 mentha long
34	7	0.7	165	10 Q8S3X6	Q8S3X6 mentha long
35	7	0.7	167	5 Q9U733	Q9U733 cryptospori
36	7	0.7	167	5 Q9G0E1	Q9G0E1 cryptospori
37	7	0.7	167	5 Q9G0C8	Q9G0C8 cryptospori
38	7	0.7	173	10 Q9S7O9	Q9S7O9 oryza sativ
39	7	0.7	183	3 Q9UTV4	Q9UTV4 schizosach
40	7	0.7	192	4 Q9Y3Z9	Q9Y3Z9 homo sapien
41	7	0.7	197	16 Q9RMR8	Q9RMR8 deinococcus
42	7	0.7	210	2 Q33570	Q33570 rhodobacter
43	7	0.7	211	16 Q931V4	Q931V4 streptomyce
44	7	0.7	215	16 Q8Z1P0	Q8Z1P0 yersinia pe
45	7	0.7	217	5 Q9V4V5	Q9V4V5 drosophila
46	7	0.7	223	10 Q941R6	Q941R6 oryza sativ
47	7	0.7	223	16 Q9ZK02	Q9ZK02 helicobacte
48	7	0.7	224	2 Q9S0D9	Q9S0D9 borrelia bu
49	7	0.7	224	16 Q93S03	Q93S03 streptomyce
50	7	0.7	226	3 Q42826	Q42826 schizosach
51	7	0.7	226	16 Q25822	Q25822 helicobacte
52	7	0.7	241	8 Q9MP30	Q9MP30 forelius ch
53	7	0.7	246	5 Q8SUT3	Q8SUT3 encephalito
54	7	0.7	247	2 Q07821	Q07821 paracoccus
55	7	0.7	248	5 Q9N9P6	Q9N9P6 leishmania
56	7	0.7	258	3 Q9HFM6	Q9HFM6 penicillium
57	7	0.7	267	17 Q8ZXA9	Q8ZXA9 pyrobaculum
58	7	0.7	275	16 Q8STF1	Q8STF1 encephalito
59	7	0.7	275	16 Q92TZ9	Q92TZ9 rhizobium m
60	7	0.7	282	16 Q8YSU3	Q8YSU3 anabaena sp
61	7	0.7	284	16 Q8U7C6	Q8U7C6 agrobacteri
62	7	0.7	285	3 Q9P4S1	Q9P4S1 penicillium
63	7	0.7	294	5 Q94295	Q94295 caenorhabdi
64	7	0.7	294	16 Q9AB93	Q9AB93 caulobacter
65	7	0.7	297	2 Q9K1F0	Q9K1F0 streptomyce
66	7	0.7	300	16 Q98BC8	Q98BC8 rhizobium l
67	7	0.7	300	16 Q8ZLB0	Q8ZLB0 yersinia pe
68	7	0.7	300	16 Q8ZAB1	Q8ZAB1 yersinia pe
69	7	0.7	300	16 Q8Z298	Q8Z298 salmonella
70	7	0.7	300	16 Q8UC61	Q8UC61 agrobacteri
71	7	0.7	300	16 Q92LJ5	Q92LJ5 rhizobium m
72	7	0.7	300	16 Q8XJBS	Q8XJBS brucella me
73	7	0.7	303	16 Q9Z799	Q9Z799 chlamydia p
74	7	0.7	305	16 Q9K1S9	Q9K1S9 chlamydia p
75	7	0.7	306	2 Q9S6E7	Q9S6E7 vibrio angu
76	7	0.7	309	4 Q9SE82	Q9SE82 homo sapien
77	7	0.7	310	16 Q8Z180	Q8Z180 yersinia pe
78	7	0.7	312	16 Q9EWZ9	Q9EWZ9 streptomyce
79	7	0.7	315	16 Q97FUI	Q97FUI clostridium
80	7	0.7	317	16 Q981S2	Q981S2 rhizobium l
81	7	0.7	318	10 Q43055	Q43055 populus kit
82	7	0.7	325	12 Q91B43	Q91B43 phocid hept
83	7	0.7	327	10 Q9CAX9	Q9CAX9 arabidopsis
84	7	0.7	327	16 Q9PCG1	Q9PCG1 ureaplasma
85	7	0.7	336	16 Q97KX8	Q97KX8 clostridium
86	7	0.7	347	10 Q8RYP3	Q8RYP3 gossypium h
87	7	0.7	350	16 Q8Z0T2	Q8Z0T2 salmonella
88	7	0.7	350	16 Q8Z8B5	Q8Z8B5 salmonella
89	7	0.7	357	5 Q8SUY1	Q8SUY1 encephalito

90	7	0.7	360	16	Q92HR6	Q92hr6 rickettsia
91	7	0.7	361	16	Q9CN76	Q9cn76 pasteurella
92	7	0.7	364	16	Q9SKA0	Q9ska0 macaca fasc
93	7	0.7	364	16	Q9FC16	Q9fc16 streptomyce
94	7	0.7	371	5	P91984	P91984 caenorhabdi
95	7	0.7	371	16	Q9CBV6	Q9cbv6 mycobacteri
96	7	0.7	371	16	Q9CBV6	Q9cbv6 mus musculu
97	7	0.7	386	11	Q91WP3	Q91wp3 mus musculu
98	7	0.7	386	16	Q96648	Q96648 mycobacteri
99	7	0.7	387	4	Q9Y4S3	Q9y4s3 homo sapien
100	7	0.7	389	16	Q9PC12	Q9pc12 xylella fas
101	7	0.7	391	16	Q9PM60	Q9pm60 staphylococ
102	7	0.7	392	11	Q9P883	Q9p883 agaricus bi
103	7	0.7	392	11	Q9CY58	Q9cy58 mus musculu
104	7	0.7	392	11	Q9VHU3	Q9vhu3 rattus norv
105	7	0.7	393	4	Q9Y367	Q9y367 homo sapien
106	7	0.7	402	4	Q9EUM4	Q9eum4 homo sapien
107	7	0.7	402	4	Q8WUHO	Q8wuh0 streptomyce
108	7	0.7	404	16	Q9AK93	Q9ak93 streptomyce
109	7	0.7	407	11	Q9DBY6	Q9dby6 mus musculu
110	7	0.7	408	4	Q9BRTY3	Q9bry3 homo sapien
111	7	0.7	409	9	Q64275	Q64275 lactococcus
112	7	0.7	410	4	Q96PC2	Q96pc2 homo sapien
113	7	0.7	413	2	Q931F7	Q931f7 priodonbac
114	7	0.7	419	16	Q8XSW3	Q8xsw3 talstonia s
115	7	0.7	422	16	Q9BWF1	Q9bwf1 homo sapien
116	7	0.7	422	16	Q9CMS4	Q9cms4 pasteurella
117	7	0.7	423	16	Q8ZD48	Q8zda4 yersinia pe
118	7	0.7	431	16	Q8YSW8	Q8ysw8 anabaena sp
119	7	0.7	434	16	Q98S36	Q98s36 galliardia
120	7	0.7	436	16	Q9XAZ7	Q9xaz7 streptomyce
121	7	0.7	438	5	Q9N948	Q9n948 crypanosoma
122	7	0.7	445	5	Q9N811	Q9n811 crypanosoma
123	7	0.7	446	5	Q9VJ92	Q9vj92 diosiphila
124	7	0.7	450	2	Q55109	Q55109 synecococc
125	7	0.7	450	10	Q9SLB8	Q9slb9 arabidopsis
126	7	0.7	450	12	Q91S68	Q91s68 planaria as
127	7	0.7	451	10	Q9MLX6	Q9mlx6 arabidopsis
128	7	0.7	452	10	Q9LWZ3	Q9lwz3 oryza sativ
129	7	0.7	468	8	Q32863	Q32863 pedionomas
130	7	0.7	471	16	Q8XZY7	Q8xzy7 talstonia s
131	7	0.7	474	16	Q96AF8	Q96af8 homo sapien
132	7	0.7	482	17	Q58773	Q58773 methanococ
133	7	0.7	495	16	Q8Y988	Q8y988 listeria mo
134	7	0.7	508	5	Q9UAR0	Q9uar0 caenorhabdi
135	7	0.7	515	10	Q82588	Q82588 arabidopsis
136	7	0.7	515	10	Q9CSM7	Q9csm7 arabidopsis
137	7	0.7	515	12	Q64784	Q64784 avian adeno
138	7	0.7	521	16	Q8XP53	Q8xp53 clostridium
139	7	0.7	524	4	Q94818	Q94818 homo sapien
140	7	0.7	530	10	Q9SG67	Q9sg67 lycopersico
141	7	0.7	530	10	Q9SG66	Q9sg66 lycopersico
142	7	0.7	530	10	Q82811	Q82811 arabidopsis
143	7	0.7	530	16	Q99XAX3	Q99xax3 staphylococ
144	7	0.7	531	10	Q8W071	Q8w071 oryza sativ
145	7	0.7	538	4	Q9H1W6	Q9h1w6 homo sapien
146	7	0.7	538	11	Q8R562	Q8r562 mus musculu
147	7	0.7	549	3	Q93956	Q93956 emeticella
148	7	0.7	558	10	Q9FM20	Q9fm20 arabidopsis
149	7	0.7	558	12	Q36296	Q36296 venezuelan
150	7	0.7	558	12	Q36293	Q36293 venezuelan

ALIGNMENTS

RESULT 1

Q9P2M2 PRELIMINARY: PRT: 580 AA.
 AC Q9P2M2: (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE KIAA1324 protein (Fragment).
 GN KIAA1324.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP TISSUE=BRAIN;
 RA MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 7:65-73(2000).
 DR EMBL; AB037745; BAA92562.1; -.
 FT NON TER
 SQ SEQUENCE 580 AA; 63365 MW; 5E63C19265CE85C CRC64;

Query Match 55.3%; Score 554; DB 4; Length 580;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	425	WMNTLPMTMETVYLSGINFEYKMGTEVAGDHIYTAAGASDNDPMILTVVPGFRPQS	484
Db	1	WMNTLPMTMETVYLSGINFEYKMGTEVAGDHIYTAAGASDNDPMILTVVPGFRPQS	60
Qy	485	VMADTENKEVARITVEETLCVNCGLYFMVGVNSRTNTPVETWKSXKQSTYIIEN	544
Db	61	VMADTENKEVARITVEETLCVNCGLYFMVGVNSRTNTPVETWKSXKQSTYIIEN	120
Qy	545	TTTSFTAFORTTTHESRKYNDVAKIYSINTVWNGVASCPCALASDVSSCTS	604
Db	121	TTTSFTAFORTTTHESRKYNDVAKIYSINTVWNGVASCPCALASDVSSCTS	180
Qy	605	CPAGYIDRDSGTSCSPNTILKAHPYGVQACVPCGPKTKNKHSLCTNDCTSRNT	664
Db	181	CPAGYIDRDSGTSCSPNTILKAHPYGVQACVPCGPKTKNKHSLCTNDCTSRNT	240
Qy	665	PTTFNPNFSLANTVTLAGSPSTSGKLYFHHFTLSLGNQGRKMSVCTDVTDLRIP	724
Db	241	PTTFNPNFSLANTVTLAGSPSTSGKLYFHHFTLSLGNQGRKMSVCTDVTDLRIP	300
Qy	725	EGSGFSKSIYAVYCOAVIIPPEVTGYKAGVSGPVSALADRLIGVTTMTLIDGITSFAL	784
Db	301	EGSGFSKSIYAVYCOAVIIPPEVTGYKAGVSGPVSALADRLIGVTTMTLIDGITSFAL	360
Qy	785	PHLESGLIPDVIFFYRSNDVTQSCSGRSTTRRCSPQTVGSGILLPPTCSDGTCDC	844
Db	361	PHLESGLIPDVIFFYRSNDVTQSCSGRSTTRRCSPQTVGSGILLPPTCSDGTCDC	420
Qy	845	NHFMESAAACPLCSVDYHAIVSSCVAGIOTTYVREPKLCSGSIISPEQRTICKT	904
Db	421	NHFMESAAACPLCSVDYHAIVSSCVAGIOTTYVREPKLCSGSIISPEQRTICKT	480
Qy	905	IDFWLKVGISAGCTAAILLVLYTCYFWKQKLEKYTSKLVNATLTKDCDLPADSCAIM	964
Db	481	IDFWLKVGISAGCTAAILLVLYTCYFWKQKLEKYTSKLVNATLTKDCDLPADSCAIM	540
Qy	965	EGEDVEDDLIFTSK 978	
Db	541	EGEDVEDDLIFTSK 554	

RESULT 2

Q8R215 PRELIMINARY: PRT: 300 AA.
 AC Q8R215:
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE Hypothetical 32.6 kDa protein (Fragment).
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (FE8-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022655; AA022655.1; -
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 300 AA; 32642 MW; 6455109C054B6CB4 CRC64;

Query Match
 Best Local Similarity 9.1%; Score 91; DB 11; Length 300;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 882 WREPKLCSGGISLPORVITCTIDFWLKVGISAGCTTALLTVLTCYFWKKQKLEKYY 941
 Db 169 WREPKLCSGGISLPORVITCTIDFWLKVGISAGCTTALLTVLTCYFWKKQKLEKYY 228

Qy 942 SKLVNATLTKODLPAPDSALMEGEDVEDD 972
 Db 229 SKLVNATLTKODLPAPDSALMEGEDVEDD 259

RESULT 3

Q96DP2 PRELIMINARY; PRT; 493 AA.

AC Q96DP2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 20, Last sequence update)
 DE CDNA FLJ31340 f1s, clone MESAN100035, weakly similar to major
 DE surface-labeled trophozoite antigen precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RN RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Saito H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hiro Y., Saito K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Maeno Y., Nagai K.,
 RA Iio T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK055502; BAB71041.1; -
 DR InterPro; IPR001881; EGF CA.
 DR SNARK; SM00179; EGF CA; 1.
 SQ SEQUENCE 493 AA; 54585 MW; 0AEBB2C19709B211 CRC64;

Query Match
 Best Local Similarity 1.5%; Score 15; DB 4; Length 493;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 GVAYTSECFCKPCT 282
 Db 43 GVAYTSECFCKPCT 57

RESULT 4

Q42206 PRELIMINARY; PRT; 97 AA.

AC Q42206;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Peroxidase (Fragment).

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 (1)
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=SEEDLING;
 RA Desprez T., Amselem J., Chiapello H., Caboche M., Hofte H.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z29133; CA82392.1; -
 DR HSSP; P00433; ZATU.
 DR InterPro; IPR002016; Peroxidase.
 DR Pfam; PF00141; peroxidase; 1.
 DR PRINTS; PR00458; PEROXIDASE.
 DR PROSITE; PS00436; PEROXIDASE 2; 1.
 FT NON_TER
 SQ SEQUENCE 97 AA; 10506 MW; A1862BE20C045EFE CRC64;

Query Match
 Best Local Similarity 0.8%; Score 8; DB 10; Length 97;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 VTLAGPS 687
 Db 82 VTLAGPS 89

RESULT 5

Q9PXT8 PRELIMINARY; PRT; 133 AA.

AC Q9PXT8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Genome polyprotein [contains: envelope glycoprotein E2/NS1 (GP68)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 NCBI_TaxID=11103;
 (1)
 RN RP SEQUENCE FROM N.A.
 RX MEDLINE-94069940; PubMed=8249288;
 RA Higashi Y., Kakumu S., Yoshioka K., Wakita T., Mizokami M., Ohba K.,
 RA Ito Y., Ishikawa T., Takayanagi M., Nagai Y.;
 RT "Dynamics of genome change in the E2/NS1 region of hepatitis C virus
 in vivo."
 RL Virology 197;659-668(1993).
 DR InterPro; IPR002531; HCV NS1.
 DR Pfam; PF01560; HCV NS1.
 DR ProDom; PD186062; HCV NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 SQ SEQUENCE 133 AA; 14623 MW; D04D3DC045350488 CRC64;

Query Match
 Best Local Similarity 0.8%; Score 8; DB 12; Length 133;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 HGFASISA 139
 Db 26 HGFASISA 33

RESULT 6

Q9CSR4 PRELIMINARY; PRT; 248 AA.

AC Q9CSR4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE AT3949120.
 GN AT3949120/T2J13.40.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Shum P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carancini P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
 RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Pham P.K., Quach H.U., Sakano H., Sakurai T., Sacou M., Seki M.,
 RA Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W.,
 RA Theologis A., Ecker J.R.,
 RT "Arabidopsis cDNA clones."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF324700; AAC40051.2; -
 DR HSSP: P00433; ZATU.
 DR InterPro: IPR02016; Peroxidase.
 DR Pfam: PF00141; Peroxidase; 1.
 DR PRINTS: PR00458; PEROXIDASE.
 DR PROSITE: PS00436; PEROXIDASE_2; 1.
 SQ SEQUENCE 248 AA; 27154 MW; 3007F7117D236BEA CRC64;

Query Match 0.8%; Score 8; DB 10; Length 248;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 680 VTLAGSPS 687
 DB 139 VTLAGSPS 146

RESULT 7
 ID 08V7G7 PRELIMINARY; PRT; 302 AA.
 AC 08V7G7;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ORF3.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 NCBI_TaxID=68887;
 [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=UT41F;
 RC MEDLINE=2184401; PubMed=11855633;
 RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
 RA Okamoto H.,
 RT "Analysis of the complete genomes of thirteen TT virus variants
 RT classified into the fourth and fifth genetic groups, isolated from
 RT viremic infants."
 RL Arch. Virol. 147:21-41(2002).
 DR EMBL: AB064603; BAB79340.1;
 DR InterPro: IPR04118; TT_ORF2.
 DR Pfam: PF02957; TT_ORF2; 1.
 SQ SEQUENCE 302 AA; 32388 MW; CD492A959881A33C CRC64;

Query Match 0.8%; Score 8; DB 12; Length 302;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 DSAESTG 152
 DB 278 DSAESTG 285

RESULT 8
 ID Q42584 PRELIMINARY; PRT; 353 AA.
 AC Q42584;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Peroxidase (EC 1.11.1.7).
 GN PRXB.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. COLUMBIA;
 RC MEDLINE=94159792; PubMed=8115548;
 RA Intaprak C., Takano M., Shimmyo A.,
 RT "Nucleotide sequence of a new cDNA for peroxidase from Arabidopsis
 RT thaliana."
 RL Plant Physiol. 104:285-286(1994).
 DR EMBL: X71794; CAA50677.1; -
 DR HSSP: P00433; ZATU.
 DR InterPro: IPR02016; Peroxidase.
 DR Pfam: PF00141; Peroxidase; 1.
 DR PRINTS: PR00458; PEROXIDASE.
 DR PROSITE: PS00435; PEROXIDASE_1; 1.
 DR PROSITE: PS00436; PEROXIDASE_2; 1.
 KM Oxidoreductase; Peroxidase.
 SQ SEQUENCE 353 AA; 38951 MW; 8AD65C72E19B10B CRC64;

Query Match 0.8%; Score 8; DB 10; Length 353;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 680 VTLAGSPS 687
 DB 139 VTLAGSPS 146

RESULT 9
 ID Q9SMU8 PRELIMINARY; PRT; 353 AA.
 AC Q9SMU8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Peroxidase (Putative peroxidase protein) (AT3949120/T2J13.40).
 GN T2J13.40.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
 RA Wewes H.W., Lemcke K., Mayer K.F.X., Quettler F., Salanoubat M.,
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
 RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
 RA Toriumi M., Yu G., Shinzaki K., Davis R.W., Ecker J.R., Theologis A.,
 RT "Full length cDNA of gene T2J13.40 (GI:6522554)."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RA	Ferretti U.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primmex C., Sezate S., Suzorov A.N., Kenton S., Lai H.S., Lin S.P., RA Qian Y., Jia H.G., Najjar F.Z., Ran Q., Zhu H., Song L., White J., RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R., RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.", RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RH	EMLL; AE006532; AKK3754.1; -.
SW	Hypothetical protein; Complete proteome.
SQ	SEQUENCE 430 AA; 48538 MW; 5BB9A2223C45B836 CRC64;
Query Match	
Best Local Similarity	0.8%; Score 8; DB 16; Length 430;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	991 RGLMDLT 998
DB	344 RGLMDLT 351
RESULT 11	
ID	092IL4 PRELIMINARY; PRT; 444 AA.
AC	092IL4
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE	TOLB protein.
GN	TOLB OR RC0406.
OS	Rickettsia conorii.
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
CC	Rickettsiaceae; Rickettsiaseae; Rickettsia.
NCBI_Taxid=781;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MALISH 7;
RX	MEDLINE=21442074; PubMed=11557893;
RA	Gedra H., Audic S., Renesto-Audifren P., Fournier P.-E., Barbe V., RA Raoulot D., Roux V., Cossart P., Weissbach J., Claverie J.-M., RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.", RL Embry; AE008605; AAL02944.1; -. DR Complete proteome.
KW	SEQUENCE 444 AA; 49080 MW; 3A0E50543E53D7F2 CRC64;
Query Match	
Best Local Similarity	0.8%; Score 8; DB 16; Length 444;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	161 PRGDYIAF 168
DB	341 PRGDYIAF 348
RESULT 12	
ID	09Z891 PRELIMINARY; PRT; 695 AA.
AC	09Z891
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, last sequence update)
DE	01-MAR-2002 (TREMBLrel. 20, last annotation update)
GN	Hypotheical protein CP0458.
OS	Chlamydia pneumoniae (Chlamydiophila pneumoniae).
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiophila.
NCBI_Taxid=83558;	
RX	STRAIN=CWL029;
RA	Kalman S., Mitchell W., Martche R., Iammel C., Fan J., Hyman R.W., RA Olinger L., Grimwood J., Davis P.W., Straub...

RL Nat. Genet. 21:385-389 (1999).
 DR EMBL: A8001630; AAD18600.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 695 AA; 78562 MW; 446CFEB1014693B CRC64;
 Query Match 0.8%; Score 8; DB 16; Length 695;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 868 VSSCVAGI 875
 DB 67 VSSCVAGI 74
 RESULT 13
 09J558 PRELIMINARY; PRT; 695 AA.
 AC 09J558.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Hypothetical protein CP00458.
 GN CP00458 OR CP0294.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OC NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Baas S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Wimmer M., Nelson W., Desoy R., Kolony J., McClary G., Salberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWR029 from USA."
 RL Nucleic Acids Res. 28:2311-2314 (2000).
 DR EMBL: A602191; AAF38151.1; -
 DR EMBL: AF002546; BAA98664.1; -
 DR TIGR: CP0294; -
 KW Hypothetical protein.
 SQ SEQUENCE 695 AA; 78471 MW; 1F9625881081B670 CRC64;
 Query Match 0.8%; Score 8; DB 16; Length 695;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 868 VSSCVAGI 875
 DB 67 VSSCVAGI 74
 RESULT 14
 042958 PRELIMINARY; PRT; 744 AA.
 AC 042958.
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Hypothetical 82.9 kDa protein Cl9G7.10C in chromosome II.
 GN SPBC1967.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetes; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: TO YEAST PAT1.
 DR EMBL: AL021839; CAA17064.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 744 AA; 82920 MW; 888E06B42FD92B5 CRC64;
 Query Match 0.8%; Score 8; DB 3; Length 744;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 LKQSGTVN 190
 DB 642 LKQSGTVN 649
 RESULT 15
 095XN6 PRELIMINARY; PRT; 77 AA.
 AC 095XN6.
 ID 095XN6.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical 8.6 kDa protein.
 GN Y71G12B.14.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Du H., Lamar B., Wohlmann P.;
 RT "The sequence of C. elegans cosmid Y71G12B."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC025726; AAK73913.1; -
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam: PF01423; Sm; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 77 AA; 8602 MW; 805A43965E96C978 CRC64;
 Query Match 0.7%; Score 7; DB 5; Length 77;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 237 RGNVLY 243
 DB 65 RGNVLY 71
 RESULT 16
 09W2P5 PRELIMINARY; PRT; 79 AA.
 ID 09W2P5

AC Q9W2P5; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CG9344 protein.
 GN CG9344.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bown B.P., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA Deason K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA DuRin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlechina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Follard J., Puri V., Reese M.G.,
 RA Reinet K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao C., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195 (2000).
 DR EMBL: AE003452; AAF4645.1; -
 DR FlyBase: FBgn0034564; CG9344.
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam: PF01423; Sm; 1.
 SQ SEQUENCE 79 AA; 9023 MW; 0480FA624ADAF5B CRC64;

Query Match 0.7%; Score 7; DB 5; Length 79;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
 DB 65 RGNVLY 71

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Putative small nuclear ribonucleoprotein polypeptide F.
 GN ATG43810.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buel C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Mayhew L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copeland G.P., Preuss D., Niernman W.C., White O., Bisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RL "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana."
 RT Nature 402:761-766 (1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC002333; BAB64025.1; -
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam: PF01423; Sm; 1.
 KW Nucleocapsid; Ribonucleoprotein.
 SQ SEQUENCE 91 AA; 9728 MW; 22DFB2C0E23BB8 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 91;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
 DB 73 RGNVLY 79

RESULT 18
 ID Q9M123 PRELIMINARY; PRT; 91 AA.
 AC Q9M123;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE U6 snRNA-associated Sm-like protein.
 GN P24316.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RX Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL138647; CAB75800.1; -
 DR InterPro: IPR001163; snRNP_Sm.
 DR Pfam: PF01423; Sm; 1.
 SQ SEQUENCE 91 AA; 9913 MW; 950E3FE402F92045 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 91;
 Best Local Similarity 100.0%; Pred. No. 63;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 RGNVLY 243
Db 73 RGNVLY 79

RESULT 19

Q9F1F2 PRELIMINARY; PRT; 93 AA.
AC O9F1F2; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, last annotation update)
DB Hypothetical 10.4 KDa protein.
GN EPO044.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Plasmid pAM373.
CC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20453452; PubMed=10998166;
RA De Boever E.H., Clewell D.B., Fraser C.M.;
RT "Enterococcus faecalis conjugative plasmid pAM373: complete nucleotide
sequence and genetic analyses of sex pheromone response."
RL Mol. Microbiol. 37:1327-1341(2000).
DR EMBL; AE002565; AAG40455.1;-.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 93 AA; 10366 MW; 344C9A25E2DD1922 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 YADKGS 289
Db 50 YADKGS 56

RESULT 20
Q9XCP1 PRELIMINARY; PRT; 100 AA.
AC Q9XCP1;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Proliferating cell nuclear antigen (Fragment).
GN PCNA.
OS Aureococcus anophagefferens.
OC Eukaryota; stramenopiles; Pelagophyceae; Aureococcus.
OX NCBI_TaxID=44056;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Pr-1;
RA Lin S.;
RT "Proliferating cell nuclear antigen in the brown tide alga."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF126735; AAD29399.1;-.
DR HSSP; P12004; IAXC.
DR InterPro; IPR000730; Pr_cel_nuc_antig.
DR Pfam; PF02747; PCNA_C; 1.
DR ProDom; PD002673; Pr_cel_nuc_antig; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 100 AA; 11104 MW; 0579A7DA2BF0C773 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 ESLGIPD 794

Db 13 ESLGIPD 19

RESULT 21

Q97RY2 PRELIMINARY; PRT; 106 AA.
AC Q97RY2; 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Hypothetical protein SP0650.
GN SP0650.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TR64;
RX MEDLINE=2157209; PubMed=11463916;
RA Tetselin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Hatt D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiolini S., Dickinson T., Hickey E.K.,
RA Holt I.B., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AE007374; AAK74796.1;-.
DR TIGR; SP0650;-.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 106 AA; 12657 MW; 4C3286B5A4B572 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 MILTLV 476
Db 1 MILTLV 7

RESULT 22
Q9N7S4 PRELIMINARY; PRT; 115 AA.
AC Q9N7S4;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
DE Possible kila0568 protein (Fragment).
GN LM28.111.
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDELIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390935; CAC00863.1;-.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 115 AA; 13150 MW; 7D3510574146C72D CRC64;

Query Match 0.7%; Score 7; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 LADRLIG 768

Db 62 LADRLIG 68

RESULT 23

ID 09M280 PRELIMINARY; PRT; 116 AA.
AC 09M280; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Hypothetical 12.7 kDa protein.
GN T2287.130.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Meiller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quettler F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138641; CAB86923.1; -
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 12696 MW; 6E43AAD0115740F6 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 434 ETTVLSG 440
DB 34 ETTVLSG 40

RESULT 24

ID 09RAN1 PRELIMINARY; PRT; 122 AA.
AC 09RAN1; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Membrane protein.
GN ORF-1.
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; beta subdivision; Methylobacillus group;
OC Methylobacillus.
OX NCBI_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=KT;
RX MEDLINE=20055654; PubMed=10589373;
RA Marchenko G.N., Marchenko N.D., Tsygankov Y.D., Chistoseedov A.Y.;
RT "Organization of threonine biosynthesis genes from the obligate
RL methylobacilli Methylobacillus flagellatus.";
DR EMBL; L78665; AAF21127.1; -
SQ SEQUENCE 122 AA; 13500 MW; 7D8E0F4621303693 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 827 PGSLLLP 833
DB 37 PGSLLLP 43

RESULT 25

ID 094045 PRELIMINARY; PRT; 124 AA.
AC 094045; 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN T13F2.2 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Swindburne J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
DR EMBL; Z81122; CAB03353.1; -
DR HSSP; P53999; 1PCF.
DR InterPro; IPR003173; PC4.
DR Pfam; PF02229; PC4; 1.
SQ SEQUENCE 124 AA; 14446 MW; 1858475E1A659D91 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 124;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 609 YYIDRDS 615
DB 87 YYIDRDS 93

RESULT 26

ID 096404 PRELIMINARY; PRT; 132 AA.
AC 096404; 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE Erythrocyte membrane protein 1 (Fragment).
GN FCRI3S1.2VAR8.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=56833;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen Q., Wahlgren M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039280; AAD02163.1; -
FT NON_TER 1
FT NON_TER 132
SQ SEQUENCE 132 AA; 15584 MW; 2532AD6D04E1BD63 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 529 KGSKGKQ 535
DB 85 KGSKGKQ 91

RESULT 27

ID 097UE3 PRELIMINARY; PRT; 134 AA.
AC 097UE3;

DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Hypothetical protein SSO3078.
 GN SSO3078.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 NCBI_Taxid=2287;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RA MEDLINE=2133296; PubMed=1142726;
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aways M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Erasmo G., Fletcher C., Gordon P.M.K.,
 RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AF006899; AK43178.1; -.
 DR InterPro; IPR002716; PIN.
 DR Pfam; PF01850; PIN; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 134 AA; 1545 MW; E0C6C1ED74E039A5 CRC64;

Query Match 0.7%; Score 7; DB 17; Length 134;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 714 CTDNVTD 720
 Db 76 CTDNVTD 82

RESULT 28
 Q9EUI6 PRELIMINARY; PRT; 138 AA.
 AC Q9EUI6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Orf40.
 OS Salmonella enterica subsp. enterica serovar Choleraesuis.
 OG Plasmid 50k virulence plasmid.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_Taxid=119912;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=RE-1;
 RA MEDLINE=21153631; PubMed=11254626;
 RA Haneida T., Okada N., Nakazawa N., Kawakami T., Danbara H.;
 RT "Complete DNA Sequence and Comparative Analysis of the 50-Kilobase
 RT Virulence Plasmid of Salmonella enterica Serovar Choleraesuis.";
 RL Infect. Immun. 69:2612-2620(2001).
 DR EMBL; AB040415; BAB20547.1; -.
 KW Plasmid.
 SQ SEQUENCE 138 AA; 16387 MW; C1E38C2757422F62 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 491 NKEVARI 497
 Db 93 NKEVARI 99
 RESULT 29
 005567

ID 005567 PRELIMINARY; PRT; 141 AA.
 AC 005567;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Hypothetical 15.8 kDa protein.
 GN MLC33.17.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 NCBI_Taxid=1769;
 RN
 RP SEQUENCE FROM N.A.
 RA Badcock K., Churche C.M.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Barrett B.G., Rajadream M.A.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9318700; PubMed=8446027;
 RA Eiglmeyer K., Honore N., Woods S.A., Caudron B., Cole S.T.;
 RT "Use of an ordered cosmid library to deduce the genomic organization
 RT of Mycobacterium leprae.";
 RL Mol. Microbiol. 7:197-206(1993).
 DR EMBL; Z94723; CAB0813.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 141 AA; 15792 MW; 0430A69020B7988 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 EFHSYEL 235
 Db 83 EFHSYEL 89

RESULT 30
 Q9HRJ4 PRELIMINARY; PRT; 159 AA.
 AC Q9HRJ4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Vng0670h.
 OG Halobacterium sp. (strain NRC-1).
 OS Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacteriaceae; Halobacterium.
 NCBI_Taxid=64091;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lauby S.R., Baliga N.S., Thorsen V., Shroga J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
 RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.V., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebbardt H., Lowe T.M., Liang P., Riley M., Hood L., Dasgupta S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AB005013; AAG19164.1; -.
 KW Complete proteome.
 SQ SEQUENCE 159 AA; 15971 MW; BCC586A96222C254 CRC64;

Query Match 0.7%; Score 7; DB 17; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 28 LLLMAGT 34
 Db 124 LLLMAGT 130

RESULT 31

Oy 090732 PRELIMINARY; PRT; 163 AA.
 ID 090732;
 AC 090732;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Oocyst wall protein (Fragment).
 OS Cryptosporidium parvum.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 NCBI_TaxID=83399;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9437830; PubMed=10508071;
 RA Sulaiman I.M., Xiao L., Lal A.A.;
 RT "Evaluation of cryptosporidium parvum genotyping techniques."; Appl. Environ. Microbiol. 65:4431-4435(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sulaiman I.M., Xiao L., Lal A.A.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161580; AAF04006.2;
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 163
 SQ SEQUENCE 163 AA; 17221 MW; 5DDAE831D52FPA CRC64;

Query Match 0.7%; Score 7; DB 5; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 621 CPNTIL 627
 Db 93 CPNTIL 99

RESULT 32

Oy 09G0D9 PRELIMINARY; PRT; 163 AA.
 ID 09G0D9;
 AC 09G0D9;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Oocyst wall protein (Fragment).
 OS Cryptosporidium muris.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 OC Cryptosporidiidae; Cryptosporidium.
 NCBI_TaxID=5808;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=34;
 RX MEDLINE=20551138; PubMed=11097936;
 RA Xiao L., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A., Lal A.A.;
 RT "Sequence Differences in the diagnostic Target Region of the Oocyst Wall Protein Gene of Cryptosporidium Parasites."; Appl. Environ. Microbiol. 66:5499-5502(2000).
 DR EMBL; AF266264; AAC39045.1;
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 163
 SQ SEQUENCE 163 AA; 17295 MW; 734B427DCFB9D19E CRC64;

Query Match 0.7%; Score 7; DB 5; Length 163;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 621 CPNTIL 627
 Db 96 CPNTIL 102

RESULT 33

Oy 08S448 PRELIMINARY; PRT; 165 AA.
 ID 08S448;
 AC 08S448;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Disease resistance-like protein 585-6 (Fragment).
 OS Mentha longifolia (Horse mint).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Lamiales; Mentha.
 NCBI_TaxID=38859;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davis T.M., Vining K.J., Smith C.A., Zhang Q.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF469686; AAL83215.1;
 FT NON_TER 1
 FT NON_TER 165
 SQ SEQUENCE 165 AA; 18180 MW; 61596CB7937AFDDP CRC64;

Query Match 0.7%; Score 7; DB 10; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 787 LESIGIP 793
 Db 87 LESIGIP 93

RESULT 34

Oy 08S3X6 PRELIMINARY; PRT; 165 AA.
 ID 08S3X6;
 AC 08S3X6;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Disease resistance-like protein 17-36 (Fragment).
 OS Mentha longifolia (Horse mint).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Lamiales; Mentha.
 NCBI_TaxID=38859;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Davis T.M., Vining K.J., Smith C.A., Zhang Q.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF474173; AAL83251.1;
 FT NON_TER 1
 FT NON_TER 165
 SQ SEQUENCE 165 AA; 18312 MW; 91BB59DD31329C2 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 165;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 787 LESIGIP 793
 Db 87 LESIGIP 93

RESULT 35
 Oy 090733 PRELIMINARY; PRT; 167 AA.
 ID 090733

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AC 09U733;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Oocyst wall protein (Fragment).
OS Cryptosporidium muris.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=5808;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99437830; PubMed=10508071;
RX Sulaiman I.M., Xiao L., Lal A.A.;
RT "Evaluation of cryptosporidium parvum genotyping techniques.";
RL Appl. Environ. Microbiol. 65:4431-4435(1999).
DR EMBL; AF161579; AAF04005.1; -.
DR InterPro; IPR02086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
FT NON TER 1
FT NON TER 1
FT SEQUENCE 167 AA; 17665 MW; DA5BAFD3434E427D CRC64;
SQ
Query Match 0.7%; Score 7; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 CPNTIL 627
DB 96 CPNTIL 102
RESULT 36
O9G0E1 PRELIMINARY; PRT; 167 AA.
ID O9G0E1
AC O9G0E1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Oocyst wall protein (Fragment).
OS OMP.
OS Cryptosporidium andersoni.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=117008;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=845;
RX MEDLINE=20551138; PubMed=11097936;
RA Xiao L., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
RA Lal A.A.;
RT "Sequence Differences in the Diagnostic Target Region of the Oocyst
RT Wall Protein Gene of Cryptosporidium Parasites.";
RL Appl. Environ. Microbiol. 66:5499-5502(2000).
DR EMBL; AF266262; AAG39043.1; -.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
FT NON TER 1
FT NON TER 1
FT SEQUENCE 167 AA; 17623 MW; 2E6AA3161B4243F7 CRC64;
SQ
Query Match 0.7%; Score 7; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 CPNTIL 627
DB 97 CPNTIL 103

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DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Oocyst wall protein (Fragment).
OS OMP.
OS Cryptosporidium serpentis.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
OX NCBI_TaxID=83999;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=754;
RX MEDLINE=20551138; PubMed=11097936;
RA Xiao L., Limor J., Morgan U.M., Sulaiman I.M., Thompson R.C.A.,
RA Lal A.A.;
RT "Sequence Differences in the Diagnostic Target Region of the Oocyst
RT Wall Protein Gene of Cryptosporidium Parasites.";
RL Appl. Environ. Microbiol. 66:5499-5502(2000).
DR EMBL; AF266275; AAG39056.1; -.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
FT NON TER 1
FT NON TER 1
FT SEQUENCE 167 AA; 17623 MW; 2E6AA3161B4243F7 CRC64;
SQ
Query Match 0.7%; Score 7; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 621 CPNTIL 627
DB 97 CPNTIL 103

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RESULT 38
O9S7O9 PRELIMINARY; PRT; 173 AA.
ID O9S7O9
AC O9S7O9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, PAC
RT clone: p071810.0."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 1, PAC
RT clone: p0705D01."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000570; BAA85199.1; -.
DR EMBL; AP000492; BAA84624.1; -.
DR SEQUENCE 173 AA; 19923 MW; 636824223DDCC29D CRC64;
SQ
Query Match 0.7%; Score 7; DB 10; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 535 QSYTYII 541
DB 131 QSYTYII 137

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RESULT 37
O9G0C8 PRELIMINARY; PRT; 167 AA.
AC O9G0C8;
AC O9G0C8;

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RESULT 39
Q9UTV4

PRELIMINARY; PRT; 188 AA.

AC Q9UTV4 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical 21.0 kDa protein (Fragment)
OS Schizosaccharomyces pombe (Fission yeast)
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_TaxID=4896;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=968 H90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RT Hirakawa Y.;
RT "Large-scale screening of intracellular protein localization in living
fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
DR EMBL; AB027973; BAAB7277.1; -
DR HSSP; P21707; 1BYN
DR InterPro; IPR000008; C2.
DR Pfam; PF00168; C2; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR SMART; SM00239; C2; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
KW Hypothetical protein.
FT NOX_TER 1
FT NOX_TER 188
SQ SEQUENCE 188 AA; 21013 MW; 59E63D8C2BED8750 CRC64;

Query Match 0.7%; Score 7; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 954 DLPADS 960
DB 121 DLPADS 127

RESULT 40
Q9Y329
AC Q9Y329; PRELIMINARY; PRT; 192 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]

RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Bartles J.R., Zheng L., Li A., Wang M.;
RT "Organization and chromosomal location of the espin gene in the
human.";
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF134401; AAD24480.1; -
FT NON_TER 1
FT NON_TER 192
SQ SEQUENCE 192 AA; 21971 MW; 44236A20760AEFF6 CRC64;

Query Match 0.7%; Score 7; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 435 TTVLSGI 441
DB 13 TTVLSGI 19

RESULT 41
Q9RWR8

PRELIMINARY; PRT; 197 AA.

AC Q9RWR8 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical protein DR0598.
GN DR0598.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Frazer C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001918; AAF10178.1; -
DR TIGR; DR0598; -
DR InterPro; IPR002886; Peptidase M37.
DR Pfam; PF01551; Peptidase M37.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 197 AA; 21348 MW; 7E0A29BC0874CC50 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 197;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IYTAGA 464
DB 179 IYTAGA 185

RESULT 42
O33570
AC O33570; PRELIMINARY; PRT; 210 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;
OC Rhodospirillum.
NCBI_TaxID=1063;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=2.4.1;
RA Patterson C.S., Donohue T.J.;
RT "Identification and characterization of putative cytochrome c
maturation genes (cymABCDG) from Rhodospirillum rubrum.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U83136; AAB61906.1; -
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran_1.
DR Prodom; PD000006; ABC_transporter; 1.
DR TIGR; TIGR01189; cymA; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN 1.
SQ SEQUENCE 210 AA; 21817 MW; 72C42BE3B1804DBA CRC64;

Query Match 0.7%; Score 7; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
412-PAGEPA 418
195-PAGEPA 201

RESULT 43

0931V4 PRELIMINARY; PRT; 211 AA.
AC 0931V4;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Putative integral membrane protein.
GN SC01316 OR SCBAC36F5.27C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D., Harris D.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
the 8 Mb streptomyces coelicolor A3(2) chromosome.";
RN (4)
RN Mol. Microbiol. 21:77-96(1996).
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Beantley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
RA Hwang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)."
RN (5)
RN Nature 417:141-147(2002).
RC EMBL; AL592292; CAC42863.1; -;
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00597; Deda; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN 1.
SQ SEQUENCE 211 AA; 22286 MW; 1A0F8EAV0072A64A CRC64;

Query Match 0.7%; Score 7; DB 16; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 787 LESTGIP 793
Db 25 LESTGIP 31

RESULT 44

0821P0 PRELIMINARY; PRT; 215 AA.
AC 0821P0;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Putative phosphoglycerate mutase (EC 5.4.2.1).
GN GPMB OR YP0045.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
NCBI_TaxID=632;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RA MEDLINE=21470413; PubMed=11586360.
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Septhalia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moulton S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RN (2)
RN Nature 413:523-527(2001).
RC EMBL; AJ414142; CAC89311.1; -;
DR InterPro; IPR001345; PG/BPGM_mutase.
DR Pfam; PF00300; PGAM; 1.
DR PROSITE; PS00175; PG_MUTASE; 1.
DR K*
SQ SEQUENCE 215 AA; 23829 MW; B59BC554434E47FB CRC64;

Query Match 0.7%; Score 7; DB 16; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 722 RIRPGES 728
Db 115 RIRPGES 121

RESULT 45

09VV45 PRELIMINARY; PRT; 217 AA.
AC 09VV45;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE CG12255 protein.
GN CG12255
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekstra R.A., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Gellera R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abilov R.M., Agdayan A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brothman P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dong L.E., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jallil M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Kechum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kul D., Lai Z.,
 RA Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Palzer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003527; AAF49477.1; -
 DR Flybase: FBgn0036618; CG12255.
 DR InterPro: IPR000618; Insect cuticle.
 DR Pfam: PF00379; Chitin bind 4; 1.
 SQ SEQUENCE 217 AA; 24162 MW; D362488EFA996A4 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 DANGETO 349
 Db 74 DANGETO 80

RESULT 46
 ID 094LR6 PRELIMINARY; PRT; 223 AA.
 AC 094LR6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE Hypothetical 23.5 kDa protein.
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Mofat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Telford T.,
 RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vankken S.B.,
 RA Uterback T.R., Feldlynn T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.,
 RT "Oryza sativa chromosome 10 BAC OSUNB0011A08 genomic sequence,"
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBD databases.
 DR EMBL: AC034258; AAK54290.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 223 AA; 23534 MW; 02C547E08745A473 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 TAAASD 466
 Db 35 TAAASD 41

RESULT 47
 ID 092K02 PRELIMINARY; PRT; 223 AA.
 AC 092K02;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DE Putative unipolypyrithogen-III synthase.
 GN HMD OR UHP1145.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 NCBI_Taxid=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Molt D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carnel G.,
 RA Tumblino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Ulang O., Taylor D.E., Vovis G.F.,
 RA Trust T.J.,
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen *Helicobacter pylori*,"
 RL Nature 397:176-180(1999).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP. ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 DR EMBL: AE001542; AAD06731.1; -
 DR InterPro: IPR002453; Beta_tubulin.
 DR Pfam: PF02602; HEM4; 1.
 DR PROSITE: PS00228; TUBULIN_B AUTOREG; 1.
 KW GTP-binding; Microtubules; Complete proteome.
 SQ SEQUENCE 223 AA; 25325 MW; E857C9D8F676D9D CRC64;

Query Match 0.7%; Score 7; DB 16; Length 223;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 973 LIFTSKN 979
 Db 38 LIFTSKN 44

RESULT 48
 ID 09S0D9 PRELIMINARY; PRT; 224 AA.
 AC 09S0D9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE Outer surface protein F.
 GN BBR42.
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OG Plasmid cp32-4.
 OC Bacteria; Spirochaetales; Spirochaetaceae; *Borrelia*.
 NCBI_Taxid=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Lathigra R.,
 RA White O., Dodson R., Hickey E.K., Gwinn M., Peterson J., van-Vugt R.,
 RA Palmer N., Haft D., Rosa P., Stevenson B.,
 RT "A bacterial genome in flux: The twelve linear and nine circular
 RT extrachromosomal DNAs in an infectious isolate of the Lyme disease
 RT spirochete *Borrelia burgdorferi*,"
 RL Mol. Microbiol. 0:0-0(1999).

DR EMBL; AE001577; AAF07488.1; -
 DR InterPro; IPR003483; OsPEF.
 DR Pfam; PF02471; OsPEF; 1.
 KW PfamId.
 SQ SEQUENCE 224 AA; 25416 MW; 4C3AD3F10DC9CD11 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 363 DLEGAVK 369
 |||||
 DB 28 DLEGAVK 34

RESULT 49
 ID Q93S03 PRELIMINARY; PRT; 224 AA.
 AC Q93S03;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative regulatory protein.
 GN SC06286 OR SCIG7.12C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kiese H.M., Denapate D., Eichner A., Cullum J.,
 RA Knaack H., Hopwood D.A.;
 RL "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL M1. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
 RA Huang C.-H., Kiese T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RL "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 CC EMBL; AL591083; CAC37887.1; -
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr. 1.
 KW DNA-binding; Transcription regulation.
 SQ SEQUENCE 224 AA; 24083 MW; B341BD44A209CB4 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 224;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 RLRLLL 30
 |||||
 DB 180 RLRLLL 186

RESULT 50
 ID Q42826 PRELIMINARY; PRT; 226 AA.
 AC Q42826;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE pdh1 protein precursor.
 GN PDH1 OR SPC1235.08C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OC NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JY336;
 RX MEDLINE=98162726; PubMed=9501995;
 RA Iba H., Takimoto M., Danjoh I., Fujiyama A.;
 RL "Identification and characterization of a novel trans-membrane protein
 gene, pdh1, from Schizosaccharomyces pombe.";
 RL DNA Res. 4:393-396(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9712;
 RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 DR EMBL; D88384; BAA2946.1; -
 DR EMBL; AL031764; CAA2112.1; -
 KW Transmembrane; Signal.
 FT FT 1 26 POTENTIAL.
 FT CHAIN 1 26 PDH1 PROTEIN.
 FT DOMAIN 27 226 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 27 41 POTENTIAL.
 FT DOMAIN 42 62 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 63 65 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 66 86 POTENTIAL.
 FT TRANSMEM 87 97 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 98 118 POTENTIAL.
 FT TRANSMEM 119 191 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 192 212 POTENTIAL.
 FT TRANSMEM 213 226 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 226 226 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 226 AA; 26021 MW; 3C71DB50ECB317B1 CRC64;

Query Match 0.7%; Score 7; DB 3; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 783 ELFHLES 789
 |||||
 DB 214 ELFHLES 220

RESULT 51
 ID Q25822 PRELIMINARY; PRT; 226 AA.
 AC Q25822;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Uroporphyrinogen III COSYNTASE (HMD).
 GN HP1224.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OC NCBI_TaxId=210;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kervatage A.R., Clayton R.A., Sutton G.C.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodgeon R., Khalak H.G., Glodek A.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Mallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT *pylori*.";
 RL Nature 388:539-547(1997).
 CC -1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT
 CC BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA
 CC CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
 CC EMBL; AE000628; AAD08269.1; -.
 DR TIGR; HP1224; -.
 DR InterPro; IPR002453; Beta_tubulin.
 DR InterPro; IPR003754; HEM4.
 DR Pfam; PF02602; HEM4; 1.
 DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
 DR GTP-binding; Hypothetical protein; Microtubules; Complete proteome.
 SQ SEQUENCE 226 AA; 25862 MW; 82BAF4B54D6AFEBF CRC64;

Query Match 0.7%; Score 7; DB 16; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 973 LIFTSKN 979
 |||||
 Db 38 LIFTSKN 44

RESULT 52
 Q9MP30 PRELIMINARY; PRT; 241 AA.
 AC Q9MP30;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Cytochrome b (Fragment).
 GN CYTB.
 OS *Forulis chalybaeus*.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Formicidae; Dolichoderinae; Forilids.
 OX NCBI_TaxID=121505;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ACLP;
 RA Chiotis M., Jermiin L.S., Crozier R.H.;
 RT "A molecular framework for the phylogeny of the ant subfamily
 RT Dolichoderinae.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: COMPONENT OF THE UBILINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIBSKS PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL; AF146718; AAF66718.1; -.
 DR InterPro; IPR000179; Cyt b b6.
 DR Pfam; PF00032; cytochrome b c; 1.
 DR Pfam; PF00033; cytochrome_b_N; 1.

DR PROSITE; PS00193; CYTOCHROME B COO; UNKNOWN 1.
 KM Electron transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane.
 FT NON_TER
 SQ SEQUENCE 241 AA; 28400 MW; 2105B5735635D3E2 CRC64;
 Qy 469 FMILTLV 475
 |||||
 Db 46 FMILTLV 52

RESULT 53
 Q8SUT3 PRELIMINARY; PRT; 246 AA.
 AC Q8SUT3;
 DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 DE Hypothetical protein ECU08_0300.
 GN ECU08_0300.
 OS *Encephalitozoon cuniculi*.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Meunier G., Thonart F.,
 RA Prensier G., Barbe V., Peyretailade E., Brotier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT *Encephalitozoon cuniculi*.";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590448; CAD26335.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 246 AA; 28355 MW; 34C9A1D609E0A946 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 246;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 828 GSLILPG 834
 |||||
 Db 49 GSLILPG 55

RESULT 54
 Q07821 PRELIMINARY; PRT; 247 AA.
 AC Q07821;
 DT 01-JUL-1997 (TRENBLREL. 04, Created)
 DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Flavoprotein (Fragment).
 GN SOXF.
 OS *Paracoccus denitrificans*.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Paracoccus.
 OX NCBI_TaxID=266;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB17;
 RX MEDLINE=95014061; PubMed=7928987;

RA Wodara C., Kostka S., Egert M., Kelly D.P., Friedrich C.;
 RT "Identification and sequence analysis of soxB gene essential for
 RT sulfur oxidation ability of Paracoccus denitrificans GB17.";
 RL J. Bacteriol. 176:6188-6191 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB17;
 RA Friedrich C.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB17;
 RX MEDLINE=97405897; PubMed=9260941;
 RA Wodara C., Bardschewsky F., Friedrich C.G.;
 RT "Cloning and characterization of sulfite dehydrogenase, two c-type
 RT cytochromes, and a flavoprotein of Paracoccus denitrificans GB17;
 RT Essential role of sulfite dehydrogenase in lithotrophic sulfur
 RT oxidation.";
 RL J. Bacteriol. 179:5014-5023 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB17;
 RA Friedrich C.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB17;
 RA Friedrich C.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X79242; CNA55826.1; -.
 DR HSP; Q06530; 1PCD.
 FT NON TER 247 247
 SQ SEQUENCE 247 AA; 26445 MW; 8F10A5B235A16621 CRC64;
 Query Match 0.7%; Score 7; DB 2; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 679 TVTLAGG 685
 DB 114 TVTLAGG 120
 RESULT 55
 Q9N9P6 PRELIMINARY; PRT; 248 AA.
 AC Q9N9P6;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE Hypothetical 27.3 kDa protein.
 GN L2802.04;
 OS Leishmania major.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A.,
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RX MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A.,

RA Barrell B.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL359774; CAB95238.2; -.
 DR EMBL: AL359683; CAC37117.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 248 AA; 27281 MW; 86E72D0E70970576 CRC64;
 Query Match 0.7%; Score 7; DB 5; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 398 PYGSYSN 404
 DB 156 PYGSYSN 162
 RESULT 56
 Q9HFW6 PRELIMINARY; PRT; 258 AA.
 AC Q9HFW6;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Lipase (Fragment).
 OS Penicillium expansum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OX NCBI_TaxID=27334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin L., Xie B.-F., Yang G.-Z., Shi Q.-Q., Xie L.-H., Wu S.-G.,
 RA Wu X.-F.;
 RT "Cloning and expression of Penicillium expansum lipase gene.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF284064; AAG22769.1; -.
 DR InterPro: IPR002921; Lipase_3.
 DR Pfam: PF01764; Lipase_3; 1.
 FT NON TER 1
 SQ SEQUENCE 258 AA; 27262 MW; 2953E19E431F9A9 CRC64;
 Query Match 0.7%; Score 7; DB 3; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 236 NRGNNVL 242
 DB 181 NRGNNVL 187
 RESULT 57
 Q8ZXAG PRELIMINARY; PRT; 267 AA.
 AC Q8ZXAG;
 DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Hypothetical protein PAE1369.
 GN PAE1369.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller U.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 RT aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
 DR EMBL: AE009818; AAL63440.1; -.
 DR InterPro: IPR003794; DUF191.

DR InterPro; IPR002029; Peptidase_S8.
 DR Pfam; PF02642; DUF191.1.
 DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 267 AA; 29602 MW; 0836222A1FE0C293 CRC64;

Query Match 0.7%; Score 7; DB 17; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 GAVKPA 372
 DB 22 GAVKPA 28

RESULT 58

08STF1 PRELIMINARY; PRT; 268 AA.

AC 08STF1
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Hypothetical protein EC01_0090 (Hypothetical protein EC01_1640).
 GN EC01_0090 OR EC01_1640.
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
 NC NCB1_Taxid=6035;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN=GB-M1;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1.
 RX MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretallade E., Brothier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.
 RT "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi."
 RL Nature 414:450-453 (2001).
 DR EMBL; AL590450; CAD25919.1; -
 DR EMBL; AL590445; CAD26684.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 268 AA; 30530 MW; 4BA693E33A4567D8 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 CKESRYH 55
 DB 176 CKESRYH 182

RESULT 59

092TZ9 PRELIMINARY; PRT; 275 AA.

AC 092TZ9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Purative modification methylase protein.
 GN HEMK2 OR RB1344 OR SMC21514.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymb (megaplasmid 2).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 NC NCB1_Taxid=382;
 DE [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.
 RT "The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
 DR EMBL; AL603646; CAC49744.1; -
 DR InterPro; IPR004556; Hemk.
 DR InterPro; IPR002052; N6_Mtase.
 DR InterPro; IPR004838; NHCtransf.1.
 DR InterPro; IPR000051; SAM_bind.1.
 DR TIGRfams; TIGR00536; hemk_fam.1.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; UNKNOWN_1.
 DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
 KW Methyltransferase; Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 275 AA; 29305 MW; EECB3460BFAF114 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 EDLEGAV 368
 DB 154 EDLEGAV 160

RESULT 60

08YSU3 PRELIMINARY; PRT; 282 AA.

AC 08YSU3
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Hypothetical protein A112989.
 GN A112989.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 NC NCB1_Taxid=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.
 RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."
 RL DNA Res. 8:205-213 (2001).
 DR EMBL; AP003591; BAB74688.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 282 AA; 31531 MW; 7EB39ADCD7A119AB CRC64;

Query Match 0.7%; Score 7; DB 16; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 KAGVSSQ 758
 DB 204 KAGVSSQ 210

RESULT 61

08U7C6 PRELIMINARY; PRT; 284 AA.

AC 08U7C6
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE ABC transporter, membrane spanning protein.

GN ATU4523 OR AGR L 692.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OC NCBI_TaxID=176299;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Seubal J.C., Kaul R., Almeida N.F. Jr., Woo L.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gilllet M., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.,
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194; Miller N., Blanchard M.,
 RA Goodner B., Hinkle G., Gattung S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Gurolo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Plangan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009380; AAL45317.1; ALT_INIT.
 DR EMBL; AE008234; AAK89920.1; -;
 KW Complete proteome.
 SQ SEQUENCE 284 AA; 30723 MW; B5EBBFA6B525F6 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 284;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 920 ALLTVL 926
 Db 257 ALLTVL 263

RESULT 62

Q9P451 PRELIMINARY; PRT; 285 AA.

ID Q9P451;
 AC Q9P451;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Alkaline lipase (EC 3.1.1.3) (Triacylglycerol lipase precursor).
 OS Penicillium cyclopium, and
 OS Penicillium expansum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryota; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OC NCBI_TaxID=60167, 27334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.cyclopium, STRAIN=PG37;
 RA Wu M., Qian Z., Min T., Sun C., Huang W.,
 RT "Cloning and sequencing of alkaline lipase cDNA from Penicillium
 RT cyclopium PG37.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.expansum, STRAIN=MMC20718;
 RA Wu M., Qian Z., Min T., Sun C., Huang W.,
 RT "Cloning and sequencing of alkaline lipase DNA from Penicillium
 RT expansum MMC20718.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.expansum, STRAIN=PF898;
 RA Lin L., Xie B.F., Shi Q.Q., Lin Q.Y., Yang G.Z., Wu X.F., Xie L.H.,
 RA Wu S.G.,
 RT "Cloning and sequencing of triacylglycerol lipase from Penicillium
 RT expansum PF898.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF274320; AAF82375.1; -;
 DR EMBL; AF286865; AAF99329.1; -;
 DR EMBL; AF330635; AAK07480.1; -;
 DR InterPro; IPR002921; Lipase_3.
 DR Pfam; PF01764; Lipase_3; 1.
 KW Hydrolyase; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 285
 FT SEQUENCE 285 AA; 30224 MW; C2D27B91C7557D14 CRC64;

Query Match 0.7%; Score 7; DB 3; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 NRGNNVL 242
 Db 208 NRGNNVL 214

RESULT 63

Q94295 PRELIMINARY; PRT; 294 AA.

ID Q94295;
 AC Q94295;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 34.3 kDa protein.
 GN T01C4.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Graves T., Wohlmann P.,
 RT "The sequence of C. elegans cosmid T01C4.";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.,
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U70858; AAB09178.1; -;
 DR InterPro; IPR002767; GPCR_Rhodopsin.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 294 AA; 34252 MW; 37760F176CC82405 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 FMILTVL 475
 Db 208 FMILTVL 214

DB 39 FMILLTV 45

RESULT 64

Q9AB93 PRELIMINARY; PRT; 294 AA.

AC Q9AB93; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Succinyl-CoA synthetase, alpha subunit.

GN CC0338.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eissen J., Heidelberg J.F., Riley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Deboy K.I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Ueberback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."

RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

RL -1 SIMILARITY: TO OTHER ALPHA SUBUNITS OF SUCCINYL-COA SYNTHETASE, OF EMBL; AB005707; AAK2325.1; -.

CC HSP; P07459; 1SCU.

DR HSP; P07459; 1SCU.

DR TIGR; CC0338; -.

DR InterPro: IPR003781; COA binding.

DR InterPro: IPR003781; COA binding.

DR Pfam; PF02629; COA binding; 1.

DR TIGRfam; TIGR01019; succoalalpha; 1.

DR PROSITE; PS01216; SUCCINYL_COA_LIG_1; 1.

KW ATP-binding; ligase; phosphorylation; tricarboxylic acid cycle; Complete proteome.

SO SEQUENCE 294 AA; 30138 MW; 2291AD957C99336A CRC64;

Query Match 0.7%; Score 7; DB 16; Length 294; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKGTE 90

DB 181 DPKGTE 187

RESULT 65

Q9KIF0 PRELIMINARY; PRT; 297 AA.

AC Q9KIF0; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE FBR1.

GN FBR1.

OS Streptomyces hygroscopicus var. ascomyceticus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=132248;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20323220; PubMed=10863099;

RA Wu K., Chung L., Revill W.P., Katz L., Reeves C.D.; "The FK520 gene cluster of streptomyces hygroscopicus var. ascomyceticus (ATCC 14891) contains genes for biosynthesis of unusual polycyclic extender units."

RL Gene 251:81-90(2000).

CC -1 SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

DR EMBL; AF255504; AAF6383.1; -.

DR InterPro: IPR000847; HTH_LYSR.

DR InterPro: IPR005119; LYSR_subst.

DR Pfam; PF00126; HTH_1; 1.

DR Pfam; PF03466; LYSR_substrate; 1.

DR PRINTS; PR00039; HTHLYSR.

DR PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.

KW DNA-binding; Transcription regulation.

SO SEQUENCE 297 AA; 32462 MW; D015FBD4C59A19D CRC64;

Query Match 0.7%; Score 7; DB 2; Length 297; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 VTLGGP 686

DB 270 VTLGGP 276

RESULT 66

Q98EC8 PRELIMINARY; PRT; 300 AA.

AC Q98EC8; 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Succinyl-CoA synthetase alpha-subunit.

GN M14303.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAF9303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpoto S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."

RT Mesorhizobium loti.

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003003; BAB50992.1; -.

DR InterPro: IPR003781; COA binding.

DR InterPro: IPR003781; COA binding.

DR Pfam; PF02629; COA binding; 1.

DR Pfam; PF00549; ligase-COA; 1.

DR TIGRfam; TIGR01019; succoalalpha; 1.

DR PROSITE; PS01216; SUCCINYL_COA_LIG_1; 1.

DR PROSITE; PS00399; SUCCINYL_COA_LIG_2; 1.

KW Complete proteome.

SO SEQUENCE 300 AA; 30861 MW; 6FD24A5A474CE034 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKGTE 90

DB 187 DPKGTE 193

RESULT 67

Q8ZLB0 PRELIMINARY; PRT; 300 AA.

AC Q8ZLB0; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

```

DE ABC superfamily (membrane), dipeptide transport protein 2.
GN DPEC OR STM3628.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AB008868; AAL22489.1; -.
DR InterPro: IPR000515; BPD transp.
DR Pfam: PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 300 AA; 3223 MW; 88E6ECF3D481F53 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AILLTVL 926
DB 275 AILLTVL 281
|||||
PRELIMINARY; PRT; 300 AA.
ID Q8ZA21
AC Q8ZA21;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dipeptide transport system permease protein.
GN DPEC OR YPO4001.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Penicill M.B., Sebailha M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Steven K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
DR EMBL; AJ141460; CAC93461.1; -.
DR InterPro: IPR000515; BPD transp.
DR Pfam: PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 300 AA; 32307 MW; F9E7F4C856E8EB13 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AILLTVL 926
DB 275 AILLTVL 281
|||||

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RESULT 69
082298
ID 082298 PRELIMINARY; PRT; 300 AA.
AC 082298;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Dipeptide transport system permease protein DPEC.
GN STY4170.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebailha M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627281; CAD07995.1; -.
DR InterPro: IPR000515; BPD transp.
DR Pfam: PF00528; BPD_transp; 1.
KW Complete proteome.
SQ SEQUENCE 300 AA; 32205 MW; 5087934A5A0857EA CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 920 AILLTVL 926
DB 275 AILLTVL 281
|||||
PRELIMINARY; PRT; 300 AA.
ID Q8UC61
AC Q8UC61;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE SucCyl1-COA synthetase alpha chain.
GN SUCD OR ATU2637 OR AGR_C4779.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21608550; PubMed=11743193;
RX Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D., Sr.,
RA Chapman P., Clendening J., Decherge G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Neester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).

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RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Houtell K., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Garsen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL; AB009211; AAL43618.1; -
 DR EMBL; AB008177; AAK8358.1; -
 KW Complete proteome.
 SQ SEQUENCE 300 AA; 31126 MW; 03101D8C32CB3CA9 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKGTE 90
 DB 187 DPKGTE 193

RESULT 71
 092LJ5 PRELIMINARY; PRT; 300 AA.
 AC 092LJ5.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Probable succinyl-CoA synthetase alpha chain protein
 DE (EC 6.2.1.5).
 GN SUCD OR R03054 OR SMC02481.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 NX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu S., Dreano S., Gloux S.,
 RA Godite T., Goffeau A., Kahn D., Kles B., Lelaure V., Masny D.,
 RA Phil T., Portetelle D., Puhler A., Purnelle B., Rameberger U.,
 RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gilbert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591792; CAC47633.1; -
 DR InterPro; IPR003781; CoA binding.
 DR InterPro; IPR003781; CoA binding.
 DR Pfam; PF02629; CoA binding; 1.
 DR Pfam; PF00549; Ligase-CoA; 1.
 DR TIGRPFAM; TIGR01019; succoAlpha; 1.
 DR PROSITE; PS01216; SUCCINYL_COA_Lig_1; UNKNOWN 1.
 DR PROSITE; PS00399; SUCCINYL_COA_Lig_2; UNKNOWN 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 300 AA; 30927 MW; FB83DA1106424C20 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKGTE 90
 DB 187 DPKGTE 193

RESULT 72

08YJES
 ID 08YJES PRELIMINARY; PRT; 300 AA.
 AC 08YJES.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Succinyl-CoA synthetase alpha chain (EC 6.2.1.5).
 GN BMEI0139.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 NX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA Delvecchio V.G., Kapral V., Redkar R.J., Patra G., Mijer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Uabonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Blzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AB009456; AAL51321.1; -
 DR InterPro; IPR003781; CoA binding.
 DR InterPro; IPR003781; CoA binding.
 DR Pfam; PF02629; CoA binding; 1.
 DR Pfam; PF00549; Ligase-CoA; 1.
 DR TIGRPFAM; TIGR01019; succoAlpha; 1.
 DR PROSITE; PS01216; SUCCINYL_COA_Lig_1; 1.
 DR PROSITE; PS00399; SUCCINYL_COA_Lig_2; UNKNOWN 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 300 AA; 31234 MW; 017C400CF7ADFB1A CRC64;

Query Match 0.7%; Score 7; DB 16; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DPKGTE 90
 DB 187 DPKGTE 193

RESULT 73
 09Z799 PRELIMINARY; PRT; 303 AA.
 AC 09Z799.
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CT580 hypothetical protein.
 GN CPN0807 OR CPJ0807.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shira M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattoni M., Kunara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA."
 RL Nucleic Acids Res. 28:2311-2314(2000).

DR EMBL; AE001662; AAD18945.1; -
 DR EMBL; AP002548; BAA99015.1; -
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 2.
 KM Complete proteome.
 SO SEQUENCE 303 AA; 33283 MW; A039571A51EB16F0 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 SKLVNNA 948
 DB 20 SKLVNNA 26

RESULT 74

ID O9KIS9 PRELIMINARY; PRT; 305 AA.

AC O9KIS9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Membrane protein, putative.
 GN CP1064.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 NCBI_TaxID=83558;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey B.K., Peterson J., Ueberback T., Berry K., Baes S.,
 RA Linher K., Weidman J., Khoult H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., Deboy R., Koloney J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002263; AAF73728.1; -
 DR TIGR; CP1064; -
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 2.
 SO SEQUENCE 305 AA; 33552 MW; 35820F888B0B97D1 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 942 SKLVNNA 948
 DB 22 SKLVNNA 28

RESULT 75

ID O56567 PRELIMINARY; PRT; 306 AA.

AC O56567;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Vibrio anguillarum virC.
 OS Vibrio anguillarum (Listonella anguillarum).
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella.
 NCBI_TaxID=55601;
 RX MEDLINE=96060845; PubMed=7590330;
 RA Milton D.V., Norqvist A., Wolf-Watz H.;
 RT "Sequence of a novel virulence-mediating gene, virC, from Vibrio
 anguillarum.";

RL Gene 164:95-100(1995).
 DR EMBL; U17054; AAA6984.1; -
 SO SEQUENCE 306 AA; 34888 MW; FBC15A2A76184429 CRC64;

Query Match 0.7%; Score 7; DB 2; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 PVLVRNI 264
 DB 134 PVLVRNI 140

RESULT 76

ID O96SE2 PRELIMINARY; PRT; 309 AA.

AC O96SE2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE CGI-55 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=96060845; PubMed=7590330;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey B.K., Peterson J., Ueberback T., Berry K., Baes S.,
 RA Linher K., Weidman J., Khoult H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., Deboy R., Koloney J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002263; AAF73728.1; -
 DR TIGR; CP1064; -
 DR InterPro; IPR000620; DUF6.
 DR Pfam; PF00892; DUF6; 2.
 SO SEQUENCE 309 AA; 34358 MW; C7A4CA08CE9A9E48 CRC64;

Query Match 0.7%; Score 7; DB 4; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 487 ADTENKE 493
 DB 169 ADTENKE 175

RESULT 77

ID O8Z180 PRELIMINARY; PRT; 310 AA.

AC O8Z180;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE LysR-family regulatory protein.
 GN YPO0631.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 NCBI_TaxID=632;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thompson N.R., Titball R.W., Holden M.T.G.,
 RA Baker S., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Prentice M.B., Baaham D., Bentley S.D., Brooks R.M., Dougan G.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis F., Dougan G.,
 RA Feltingworth T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
 RA Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL; AJ414143; CAC89485.1; -
 DR InterPro; IPR000847; HTH_LysR.
 DR InterPro; IPR005119; LysR_subst.
 DR InterPro; IPR003662; sub_transporter.

DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp.1.
 DR PROSITE: PS00402; BPD_TRANS_INN_MEMBER, UNKNOWN_1.
 DR Complete proteome.
 SW SEQUENCE 317 AA; 33247 MW; 747A2DDE3C61AEC2 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 761 SLADRLLI 767
 |||||
 Db 126 SLADRLLI 132

RESULT 81

Q43055 PRELIMINARY; PRT; 318 AA.
 AC Q43055;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Peroxidase (EC 1.11.1.7).
 GN PRXA1.
 OS Populus kitakamiensis (Aspen).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Malpighiales; Salicaceae; Populus.
 OC NCBI_TaxID=3698;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93169019; PubMed=7764045;
 RA Kawai S., Matsumoto Y., Kajita S., Yamada K., Katayama Y.,
 RA Morishoshi N.;
 RT "Nucleotide sequence for the genomic DNA encoding an anionic
 RT peroxidase gene from a hybrid poplar, Populus kitakamiensis.";
 RL Biosci. Biotechnol. Biochem. 57:131-133(1993).
 DR EMBL: D11102; BAA01877.1; -.
 DR HSSP: P00433; 2ATU.
 DR InterPro: IPR002016; Peroxidase.
 DR Pfam: PR00141; peroxidase.1.
 DR PRINTS: PR00458; PEROXIDASE.
 DR PROSITE: PS00435; PEROXIDASE_1; 1.
 DR PROSITE: PS00436; PEROXIDASE_2; 1.
 DR Oxidoreductase; Peroxidase.
 SW SEQUENCE 318 AA; 34172 MW; 14838148CD6076E3 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 680 VTLAGGP 686
 |||||
 Db 129 VTLAGGP 135

RESULT 82

Q91E43 PRELIMINARY; PRT; 325 AA.
 AC Q91E43;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Ue2 homologue (fragment).
 GN US2.
 OS Phocid herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OC NCBI_TaxID=47418;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=PB84;
 RA Martina B., Osterhaus A.D.M.E., Harder T.C.;

RT "Identification and analysis of immunogenicity of the glycoprotein D
 RT equivalent within the unique short segment of phocid herpesvirus-1.";
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ290955; CAC51462.1; -.
 DR InterPro: IPR003485; Ue2_Unk.
 DR Pfam: PF02476; US2; 1.
 DR NON_TER 325 325
 SW SEQUENCE 325 AA; 35995 MW; 2EF22B8FB483D1B9 CRC64;

Query Match 0.7%; Score 7; DB 12; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 887 LCSSGIS 893
 |||||
 Db 287 LCSSGIS 293

RESULT 83

Q9CAX9 PRELIMINARY; PRT; 327 AA.
 AC Q9CAX9;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Hypothetical 37.6 kDa protein.
 GN F24K9.15.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RX Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
 RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Boutry M., Grivell L.A., Maché R., Puigdomenech P.,
 RA De Simone V., Chouine N., Artiguenave F., Robert C., Brotier P.,
 RA Wincker P., Catolico L., Weisenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbech E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T., H., Nordstiek B.,
 RA Reichelt J., Scharte M., Schoen O., Bargues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Hauro C., Puttenle B., Maury D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cotellet A., Casasuberta E.,
 RA Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Ruid S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Ulteback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maltl R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Saenmoto S., Kimura T., Igesawa K., Kawashima K., Kishida A.,
 RA Nakayama S., Kohara M., Matsumoto M., Matsumoto K., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822(2000).
 RL EMBL: AC008153; AKG51446.1; -.
 DR InterPro: IPR005299; Methyltransf_6.
 DR Pfam: PF03492; Methyltransf_6; 1.
 KW Hypothetical protein.
 SW SEQUENCE 327 AA; 37575 MW; 8B3FD25A11B8D700 CRC64;

Query Match 0.7%; Score 7; DB 10; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 KPVLYRN 263

Db 3 KPVLYRN 9

RESULT 84

Q9PQGI PRELIMINARY; PRT; 327 AA.

AC Q9PQGI; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN U0330.

OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

OC Mycoplasmataceae; Ureaplasma.

OX NCBI_TaxID=134821;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SSROVAR 3; PubMed=11048724;

RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,

Caswell G.H.;

RT "The complete sequence of the mucosal pathogen Ureaplasma

urealyticum.";

RL Nature 407:757-762(2000).

DR EMBL; AB002130; AAF30739.1; -

KM Hypothetical protein; Complete proteome.

SO SEQUENCE 327 AA; 38114 MW; 321275386DAF61B7 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 327;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 469 FMILTV 475

Db 170 FMILTV 176

RESULT 85

Q97KX8 PRELIMINARY; PRT; 336 AA.

AC Q97KX8;

DT 01-OCT-2001 (TREMBlrel. 18, Created)

DT 01-JUN-2002 (TREMBlrel. 18, Last sequence update)

DE Perichrome transport permease.

GN CAC0788.

OS Clostridium acetobutylicum.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Clostridiales; Clostridiaceae; Clostridium.

OX NCBI_TaxID=1488;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE=21359325; PubMed=1146286;

RA Neilling J., Berton G., Omeichenko M.V., Makarova K.S., Zeng Q.,

Atkinson R.L., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Bennett G.N., Koonin E.V., Doucette-Stamm L., Soucaille P., Daly M.J.,

"Genome sequence and comparative analysis of the solvent-producing

bacterium Clostridium acetobutylicum.";

RT J. Bacteriol. 183:4823-4838(2001).

DR EMBL; AB007594; AAK78764.1; -

DR InterPro; IPR000522; FeCD.

DR Pfam; PF01032; FeCD; 1.

DR ProDom; PD001557; FeCD; 1.

KM Complete proteome.

SO SEQUENCE 336 AA; 36552 MW; 1BC0BC10C47B0F34 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 336;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 921 ILTVLT 927

Db 19 ILTVLT 25

RESULT 86

Q8RVP3 PRELIMINARY; PRT; 347 AA.

AC Q8RVP3;

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Bacterial-induced peroxidase (EC 1.11.1.7).

GN PODSH1.

OS Gossypium hirsutum (Upland cotton).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Malvales; Malvaceae; Gossypium.

OX NCBI_TaxID=3635;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. REBA B50; TISSUE=2 WEEK OLD COTYLEDONS;

RA Delannoy E., Patil M., Essenberg M., Jalloul A., Marney P.,

Daniel J.-F., Geiger J.-P., Nicole M.;

RT "Gossypium hirsutum bacterial-induced peroxidase (podSH1).";

DR EMBL; AF48305; AAL92037.1; -

KM Peroxidase; Oxidoreductase.

SO SEQUENCE 347 AA; 37407 MW; 51B68CA3CCE7F0BB CRC64;

Query Match 0.7%; Score 7; DB 10; Length 347;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 681 TLGGPS 687

Db 137 TLGGPS 143

RESULT 87

Q8ZQT2 PRELIMINARY; PRT; 350 AA.

AC Q8ZQT2;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 3-deoxy-D-arabinoheptulosate-7-phosphate synthase (DAHPSynthetase,

phenylalanine repressible) (EC 4.1.2.15).

GN AROG OR SPM0760.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=L72 / SCSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,

Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium

LT2.";

RL Nature 413:852-856(2001).

DR EMBL; AB008731; AAL19699.1; -

DR InterPro; IPR001785; DAHP_synth.

DR Pfam; PF00793; DAHP_synth.1; 1.

DR ProDom; PD005060; DAHP_synth.1.

DR TIGR0034; atofGH; 1.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 350 AA; 37856 MW; D79AC095B456A147 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 AGEFLDM 103
 |||||
 Db 141 AGEFLDM 147

RESULT 88
 Q828B5 PRELIMINARY; PRT; 350 AA.
 AC Q828B5;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE Phospho-2-dehydro-3-deoxyheptanate aldolase (DAH synthetase)
 DE phenylalanine repressible.
 GN STY0801.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE-21534947; PubMed-11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaiha M.,
 RA Baker S., Basham D., Brooks R.M., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gara P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL: AL627268; CAD05217.1; -;
 DR InterPro: IPR001785; DAHP synth.
 DR Pfam: PF00793; DAHP synth_1; 1.
 DR ProDom: PD005060; DAHP synth; 1.
 DR TIGR0034; atofGH; 1.
 KW Complete proteome.
 SQ SEQUENCE 350 AA; 37868 MW; C764207BBA65FE7 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 AGEFLDM 103
 |||||
 Db 141 AGEFLDM 147

RESULT 89
 Q85UY1 PRELIMINARY; PRT; 357 AA.
 AC Q85UY1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein ECU07_1170.
 GN ECU07_1170.
 OS Encephalitozoon cuniculi.
 OC Eukaryote; Microsporidia; Unikaryonidae; Encephalitozoon.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=GB-M1;
 RA Genoscope; (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL Submitted
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE-21576510; PubMed-11719806;
 RA Katinka M.D., Duprat S., Cornillon E., Metenier G., Thomarat P.,
 RA Prensier G., Barbe V., Peyretailade E., Broctier P., Winkler P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi.";
 RL Nature 414:450-453(2001).
 DR EMBL: AL590447; CAD25650.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 357 AA; 40257 MW; 715D55ED5BC2414 CRC64;

Query Match 0.7%; Score 7; DB 5; Length 357;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 663 NTPRTF 669
 |||||
 Db 166 NTPRTF 172

RESULT 90
 Q92HR6 PRELIMINARY; PRT; 360 AA.
 AC Q92HR6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Similar to microcin C7 self-immunity protein.
 GN MCCP2 OR RC0705.
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MALISH 7;
 RX MEDLINE-21442074; PubMed-11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
 RL Science 293:2093-2098(2001).
 DR EMBL: AB008629; AAL03243.1; -;
 DR InterPro: IPR003507; UPF0094.
 DR Pfam: PF02016; UPF0094; 1.
 KW Complete proteome.
 SQ SEQUENCE 360 AA; 40394 MW; B94412DFC9831C95 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 360;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 874 GIOKTY 880
 |||||
 Db 5 GIOKTY 11

RESULT 91
 Q9CN76 PRELIMINARY; PRT; 361 AA.
 AC Q9CN76;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE AroG.
 GN AROG OR PM0563.

OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxID=147;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.,
 RT "Complete genomic sequence of Pasteurella multocida Pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
 DR EMBL; AB06092; AAK02647.1; -.
 DR HSSP; P00886; 1QR7.
 DR InterPro; IPR001785; DAHP_synth1.
 DR Pfam; PF00783; DAHP_synth_1; 1.
 DR Prodom; PD005060; DAHP_synth; 1.
 DR TIGRFAMs; TIGR00034; atofGH; 1.
 KW Complete proteome.
 SQ SEQUENCE 361 AA; 40132 MW; 4B78F085186C1B2E CRC64;

Query Match 0.7%; Score 7; DB 16; Length 361;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 AGEFLDM 103
 Db 148 AGEFLDM 154

RESULT 92
 ID 095KAO PRELIMINARY; PRT; 364 AA.
 AC 095KAO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical 39.3 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MEDULLA OBLONGATA;
 RA Osada N., Hida M., Kuwada J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB063042; BAB60776.1; -.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 364 AA; 39316 MW; 46F7998483BFE746 CRC64;

Query Match 0.7%; Score 7; DB 6; Length 364;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 412 PAGTEPA 418
 Db 350 PAGTEPA 356

RESULT 93
 ID 09FC16 PRELIMINARY; PRT; 364 AA.
 AC 09FC16;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative secreted protein.

GN SC05202 OR 28C3B6.26.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.; and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147 (2002).
 DR EMBL; AL390968; CAC01332.1; -.
 DR InterPro; IPR001478; PDZ.
 DR SMART; SM00228; PDZ; 1.
 SQ SEQUENCE 364 AA; 38181 MW; 8900C095D03C17B1 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 364;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 911 VGISAGT 917
 Db 232 VGISAGT 238

RESULT 94
 ID P91984 PRELIMINARY; PRT; 371 AA.
 AC P91984;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE C50B6.10 protein.
 GN C50B6.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Rhabditinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Percy C.M.;
 RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RL investigating biology."
 DR Science 282:2012-2018(1998).
 DR EMBL; Z81050; CAB02859.1; -
 DR InterPro; IPR003002; 7TM_chemol.
 DR InterPro; IPR000168; 7TM_nematode.
 DR Pfam; PF01461; 7tm_4; 1.
 SQ SEQUENCE 371 AA; 42447 MW; 872EEC3780B43CD CRC64;

Query Match 0.7%; Score 7; DB 5; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 515 VGVNSRT 521
 DB 360 VGVNSRT 366

RESULT 95
 Q9CBV6 PRELIMINARY; PRT; 371 AA.
 AC Q9CBV6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE l-alanine dehydrogenase.
 GN ALD OR ML1532.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxId=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Bigmeyer K., Parthill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,
 RA Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrett B.G.;
 RT "Massive gene decay in the leprosy bacillus."
 RL Nature 409:1007-1011(2001).
 CC -i- COFACTOR: FAD (BY SIMILARITY).
 DR EMBL; AL583922; CAC30483.1; -
 DR HSSP; Q60164; 1H2Z.
 DR Leproma; ML1532; -
 DR InterPro; IPR004002; ALADH_PNT.
 DR InterPro; IPR001327; FAD_PYT_redox.
 DR InterPro; IPR000205; NAD_binding.
 DR Pfam; PF01262; ALADH_PNT; 1.
 DR PRINTS; PRO0368; FADPFR.
 DR TIGRPFAM; TIGR00518; aladh_1.
 DR PROSITE; PS00836; ALADH_PNT_1; 1.
 DR PROSITE; PS00837; ALADH_PNT_2; 1.
 DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 371 AA; 38845 MW; 35425DE604EF8199 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 DLGAVK 369
 DB 224 DLGAVK 230

RESULT 96
 Q9CRR7

ID Q9CRR7 PRELIMINARY; PRT; 377 AA.
 AC Q9CRR7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE MAD homolog 5 (Drosophila) (Fragment).
 GN MADH5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=EMERYONIC HEAD;
 RX MEDLINE=21085660; PubMed=1217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Holtman M., Hume D.A., Kamlya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK018077; BAB31063.1; -
 DR HSSP; Q92940; 1MDH.
 DR MGD; MGI:1328787; Madh5.
 DR InterPro; IPR001132; Dwarf1n.
 DR InterPro; IPR003619; Dwarf1n_A.
 DR InterPro; IPR004863; MH1.
 DR Pfam; PF03165; MH1; 1.
 DR Pfam; PF03166; MH2; 1.
 DR SMART; SM00523; DWA; 1.
 DR SMART; SM00524; DWA; 1.
 FT NON_TER
 SQ SEQUENCE 377 AA; 42204 MW; 8305E1452D025DE CRC64;

Query Match 0.7%; Score 7; DB 11; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 FHSVELN 236
 DB 339 FHSVELN 345

RESULT 97
 Q91WP3 PRELIMINARY; PRT; 386 AA.
 ID Q91WP3;
 AC Q91WP3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Similar to RIKEN CDNA 1200009K13 gene.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SALIVARY GLAND;
 RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013665; AAH13665.1; -
 SQ SEQUENCE 386 AA; 42235 MW; A22F5DBE68F72CB CRC64;

Query Match 0.7%; Score 7; DB 11; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 ADTENKE 493
 |||||
 Db 246 ADTENKE 252

RESULT 98

069648 PRELIMINARY; PRT; 386 AA.
 AC 069648;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DE Putative anion transporting ATPase (Hypothetical protein MT3782).
 GN RV3680 OR MT025.028 OR MT3782.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1773;
 RX MEDLINE=98295987; PubMed=9634230;
 RC STRAIN=H37RV;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Baccocck K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Stulson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M., Hatt D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains." to the EMBL/GenBank/DBJ databases.
 RL Submitted (APR-2001)
 DR EMBL; AL022121; CAA18002.1; -
 DR EMBL; AE007175; AAK48149.1; -
 DR TIGR; MT3782; -
 DR TubercuList; RV3680; -
 DR InterPro; IPR003348; AtsA_ATPase.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 386 AA; 41404 MW; A8BD2D31A4620B5 CRC64;

Query Match 0.7%; Score 7; DB 16; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 RLRLIL 30
 |||||
 Db 178 RLRLIL 184

RESULT 99
 091453 PRELIMINARY; PRT; 387 AA.
 ID 091453

AC 091453;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Hypothetical 42.4 kDa protein (PAI-1 mRNA-binding protein).
 GN DKFZP564M2423.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRNIN;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wieman S., Weil B., Wellenreuther R., Gassenhuber J., Glaser S.,
 RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Mewes H.W., Oesterweider B., Obermaler B., Tampe J., Heubner D.,
 RA Wandt R., Korn B., Klein M., Poustka A.;
 RA "Towards a Catalog of Human Genes and Proteins: Sequencing and
 RT Analysis of 500 Novel Complete Protein Coding Human cDNAs."
 RL Genome Res. 11:422-435(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL080119; CAB45718.1; -
 DR EMBL; BC017449; AAH17449.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 387 AA; 42426 MW; 8C47134D22C1CCFA CRC64;

Query Match 0.7%; Score 7; DB 4; Length 387;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 ADTENKE 493
 |||||
 Db 247 ADTENKE 253

RESULT 100
 09PC12 PRELIMINARY; PRT; 389 AA.
 ID 09PC12
 AC 09PC12;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Porphyryrin biosynthesis protein.
 GN XF1797.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Keinich F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvaranga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Brites M.R.S.,
 RA Bueno M.R.P., Colombo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Pachcani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miranda E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,

RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Mnaní A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pequeiro J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffé D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zeldandis J., Zubal J.C.,
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
 RL Nature 406:151-159(2000).
 DR EMBL; AE004001; AAF84605.1; -.
 DR InterPro; IPR001440; TPR.
 KM Complete proteome.
 SQ SEQUENCE 389 AA; 44436 MW; 2459773D3632925 CRC64;

Query Match

0.7%; Score 7; DB 16; Length 389;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 988 LPPRGLL 994
 |||||
 DB 181 LPPRGLL 187

Search completed: April 22, 2003, 15:35:32
 Job time : 72 secs